

Amendments to the Specification:

Please replace the descriptions for Figures 3 and 4 which appear on page 5 with the following descriptions:

Fig. 3. Alignment of proteins LbpB of strain BNCV (SEQ ID NO:2) and TbpB of strain B16B6 (SEQ ID NO:12). Identical amino acids are marked by dashes. The numbers to the right indicate the positions of amino acids. Gaps (-) were introduced to achieve optimal alignment. Peptides used to immunise mice are indicated above the sequence of LbpB (SEQ ID NO:2). Two stretches, rich in negatively charged residues are underlined. The putative signal peptidase II cleavage site is shown with an arrow above the sequence.

Fig. 4. Sequence of the promoter area upstream of *lbpB* (SEQ ID NO:11). The translation initiation site (ATG) is marked in bold. The ribosome binding site, and the putative -10 and -35 boxes are underlined (thick line and thin lines respectively). The putative Fur box is boxed.

Please replace the description for Figure 9 which appears on page 6 with the following description:

Fig. 9. Alignment of the LbpB proteins from five meningococcal strains: BNCV (SEQ ID NO: 2); M981 (SEQ ID NO:4); H44/76 (SEQ ID NO:6); M990 (SEQ ID NO: 8); and 881607 (SEQ ID NO:10). The alignment was performed with the CLUSTAL program (PC Gene, IntelliGenetics), and optimized by hand. Numbers to the right indicate the positions of the amino acids. Gaps (-) were introduced to achieve optimal alignment. Positions where all five sequences are identical, are marked with *.